G.Ewoldt

#30
1/2/01
1644 /hFL

ENTERED

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        RAW SEQUENCE LISTING              DATE: 01/02/2001
        PATENT APPLICATION:  US/08/756,018C      TIME: 10:20:46

        Input Set : A:\ES.txt
        Output Set: N:\CRF3\01022001\H756018C.raw

   4 <110> APPLICANT: Brian Seed
   5         Tara Pouyani
   7 <120> TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES
   8         AND METHODS
  10 <130> FILE REFERENCE: 00786/284002
  12 <140> CURRENT APPLICATION NUMBER: 08/756,018C
  13 <141> CURRENT FILING DATE: 1996-11-25
  15 <150> PRIOR APPLICATION NUMBER: 60/000,213
  16 <151> PRIOR FILING DATE: 1995-06-14
  18 <150> PRIOR APPLICATION NUMBER: 08/661,960
  19 <151> PRIOR FILING DATE: 1996-06-12
  21 <160> NUMBER OF SEQ ID NOS: 17
  23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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  26 <211> LENGTH: 10
  27 <212> TYPE: PRT
  28 <213> ORGANISM: Homo sapiens
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  36 <211> LENGTH: 18
  37 <212> TYPE: PRT
  38 <213> ORGANISM: Homo sapiens
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  55 Leu Leu Ala Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr Leu Asp
  56             20               25               30
  57 Tyr Asp Phe Leu Pro Glu Thr Glu Pro Pro
  58             35               40
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  62 <211> LENGTH: 20
  63 <212> TYPE: PRT
  64 <213> ORGANISM: Homo sapiens
  66 <400> SEQUENCE: 4
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  69 Leu Pro Glu Thr
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PATENT APPLICATION: US/08/756,018C   TIME: 10:30:46

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74 <211> LENGTH: 20
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81 Leu Pro Glu Thr
82              20
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86 <211> LENGTH: 20
87 <212> TYPE: PRT
88 <213> ORGANISM: Homo sapiens
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93 Leu Pro Glu Ala
94              20
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98 <211> LENGTH: 20
99 <212> TYPE: PRT
100 <213> ORGANISM: Homo sapiens
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116 ggtgtccagt cccaggtgca gctggtgcag tctgggctg aggtgaagaa gcctgggtcc      120
117 tcggtgaagg tctcctgcaa ggcttctgga ggcaccttca gcagctatgc tatcagctgg      180
118 gtgcgacagg cccctggaca agggcttgag tggatgggga ggatcatccc tatctttggt      240
119 acagcaaact acgcacagaa gttccagggc agagtcacga ttaccgcgga cgaatccacg      300
120 agcacagcct acatggagct gagcagcctg agatctgagg acacggccgt gtattactgt      360
121 gcgagagata atggagcgta ttgtagtggt ggtagctgct actcggctg gttcgacccc      420
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123 ggcaggccag gcctgacctt ggctttgggg caggagggg gctaaggtgu ggcaggtggc      540
124 gccagcaggt gcacacccaa tgcccatgag cccagacact ggacgctgaa cctcgcggac      600
125 agttaagaac cc gggggcct ctgcgcctgg gcccagctct gtcccacacc gcggtcacat      660
126 ggcaccacct ct ttgcagc ctccaccaag ggcccatcgg tcttccccct ggcaccctcc      720
127 tccaagaqca cctctggggg cacagcggcc ctgggctgcc tggtcaagga ctacttcccc      780
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129 gctgtcctac agtcctcagg actctactcc ctcagcagcg tggtgaccgt gccctccagc      900
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Input Set : A:\ES.txt
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132 agcgctcctg cctggacgca tcccggctat gcagccccag tccagggcag caaggcaggc  1080
133 cccgtctgcc tcttcacccg gagcctctgc ccgcccacct catgctcagg gagagggtct  1140
134 tctggcttt  tcccaggctc tgggcaggca caggctaggt gcccctaacc caggccctac  1200
135 acacaaaggg gcaggtgctg ggctcagacc tgccaagagc catatccggg aggaccctgc  1260
136 ccctgaccta agcccacccc aaaggccaaa ctctccactc cctcagctcg gacaccttct  1320
137 ctcctcccag attccagtaa ctcccaatct tctctctgca gagcccaaat cttgtgacaa  1380
138 aactcacaca tgcccaccgt gcccaggtaa gccagcccag ggctcgccct ccagctcaag  1440
139 gcgggacagg tgccctagag tagcctgcat ccaggacag  gcccagcccag ggtgctgaca  1500
140 cgtccacctc catctcttcc tcagcacctg aactcctggg gggaccgtca gtcttcctct  1560
141 tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc acatgcgtgg  1620
142 tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg  1680
143 aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg taccgggtgg  1740
144 tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac aagtgcaagg  1800
145 tctccaacaa agccctccca gcccccatcg agaaaaccat ctccaaagcc aaaggtggga  1860
146 cccgtggggt gcgagggcca catggacaga ggccggctcg gcccaccctc tgccctgaga  1920
147 gtgaccgctg taccaacctc tgtcctacag ggcagccccg agaaccacag gtgtacaccc  1980
148 tgcccccatc ccgggatgag ctgaccaaga accaggtcag cctgacctgc ctggtcaaag  2040
149 gcttctatcc cagcgacatc gccgtggagt gggagagcaa tgggcagccg gagaacaact  2100
150 acaagaccac gcctcccgtg ctggactccg acggctcctt cttcctctac agcaagctca  2160
151 ccgtggacaa gagcaggtgg cagcagggga acgtcttctc atgctccgtg atgcatgagg  2220
152 ctctgcacaa ccactacacg cagaagagcc tctccctgtc tccgggtaaa tgagtgcgac  2280
153 ggccggc                                                             2287
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164              20                  25                  30
165 Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala
166          35                  40                  45
167 Ser Gly Gly Thr Phe Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala
168      50                  55                  60
169 Pro Gly Gln Gly Leu Glu Trp Met Gly Gly Ile Ile Pro Ile Phe Gly
170 65                  70                  75                  80
171 Thr Ala Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala
172              85                  90                  95
173 Asp Glu Ser Thr Ala Arg Asp Asn Gly Ala Tyr Cys Ser Gly Gly Ser
174             100                 105                 110
175 Cys Tyr Ser Gly Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr
176         115                 120                 125
177 Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
178     130                 135                 140
179 Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
180 145                 150                 155                 160
181 Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
```

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182                165              170              175
183 Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
184            180              185              190
185 Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Asp Lys
186        195              200              205
187 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
188    210              215              220
189 Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
190 225            -    230              235              240
191 Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
192            245              250              255
193 Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
194            260              265              270
195 Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
196        275              280              285
197 Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
198        290              295              300
199 His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
200 305              310              315              320
201 Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
202            325              330              335
203 Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
204            340              345              350
205 Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
206        355              360              365
207 Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
208        370              375              380
209 Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
210 385              390              395              400
211 Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
212            405              410              415
213 Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
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220 <211> LENGTH: 1894
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227 ggcaagtggt tttatatcgc atcggccttt cgaaacgagg agtacaataa gtcggttcag     180
228 gagatccaag caaccttctt ttacttcacc cccaacaaga cagaggacac gatcttctc     240
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232 gggctgtctg tctatgctga caagccagag acgaccaagg agcaactggg agagttctac     480
233 gaagctctcg actgcttgcg cattcccaag tcagatgtcg tgtacaccga ttggaaaaag     540
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234 gataagtgtg agccactgga gaagcagcac gagaaggaga ggaaacagga ggagggggaa     600
235 tcggatcccg agggtgagta ctaagcttca gcgctcctgc ctggacgcat cccggctatg     660
236 cagcccaagt ccagggcagc aaggcaagcc ccgtctgcct cttcacccgg agcctctgcc     720
237 cgcccactc atgctcaggg agagggtctt ctgacttttt cccaggctct gggcaggcac     780
238 aggctaggtg cccctaaccc aggccctgca cacaaagggg cagtgctgg gctcagacct     840
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255 cgtcttctca tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaagagcct    1860
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267              20                  25                  30
268 Asn Ala Thr Leu Asp Gln Ile Thr Gly Lys Trp Phe Tyr Ile Ala Ser
269              35                  40                  45
270 Ala Phe Arg Asn Glu Glu Tyr Asn Lys Ser Val Gln Glu Ile Gln Ala
271      50                  55                  60
272 Thr Phe Phe Tyr Phe Thr Pro Asn Lys Thr Glu Asp Thr Ile Phe Leu
273 65                  70                  75                  80
274 Arg Glu Tyr Gln Thr Arg Gln Asp Gln Cys Ile Tyr Asn Thr Thr Tyr
275                  85                  90                  95
276 Leu Asn Val Gln Arg Glu Asn Gly Thr Ile Ser Arg Tyr Val Gly Gly
277                  100                 105                 110
278 Gln Glu His Phe Ala His Leu Leu Ile Leu Arg Asp Thr Lys Thr Tyr
279              115                 120                 125
280 Met Leu Ala Phe Asp Val Asn Asp Glu Lys Asn Trp Gly Leu Ser Val
281      130                 135                 140
282 Tyr Ala Asp Lys Pro Glu Thr Thr Lys Glu Gln Leu Gly Glu Phe Tyr
283 145                 150                 155                 160
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VERIFICATION SUMMARY
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